Claims

1. A versatile method of identifying genes having invariant peptides as functional signatures in a genome using software GeneDecipher, said method comprising steps of:
    a. generating peptide libraries from the known genomes with peptide of length 'N' computationally arranged in an alphabetical order,
    b. artificially translating the test genome to obtain peptide,
    c. identifying the reading frames in the peptide on the basis of overlappings with the peptide libraries,
    d. converting each peptide sequence into an alphanumeric sequence with one corresponding to each reading frame,
    e. training Artificial Neural Network (ANN) with sigmoidal learning function to the alphanumeric sequence,
    f. deciphering the protein coding regions in the test genome, and
    g. identifying invariant peptides serving as functional signatures.
2. A method as claimed in claim 1, wherein the ANN has one or more input layer, one or more hidden layer with varying number of neurons, and one or more output layer.
3. A method as claimed in claim 1, wherein the number of neurons is preferably 30.
4. A method as claimed in claim 1, wherein the length of the 'N' is 4 or more.
5. A method as claimed in claim 1, wherein the sigmoidal learning function has five parameters comprising total score, mean, fraction of zeroes, maximum continuous non-zero stretch, and variance.
6. A method as claimed in claim 1, wherein the method identified conserved peptide motifs of SEQ ID Nos. 174 to 240.

1. AAQSIGEPGTQLT
2 AGDGTTTAT
3. AGRHGNKG
4. AHIDAGKTTT
5. CPIETPEG
6. DEPSIGLH
7. DEPTSALD
8. DEPTTALDVT
9. DHAGIATQ
10. DHPHGGGEG

11. DLGGGTFD
12. DVLDTWFSS
13. ERERGITI
14. ERGITITSAAT
15. ESRRIDNQLRGR
16. FSGGQRQR
17. GEPGVGKTA
18. GFDYLRDN
19. GHNLQEHS
20. GIDLGTTNS
21. GINLLREGLD
22. GIVGLPNVGKS
23. GKSSLLNA
24. GLTGRKIIVDTYG
25. GPPGTGKTLLA
26. GPPGVGKT
27. GSGKTTLL
28. GTRIFGPV
29. IDTPGHVDFT
30. IIAHIDHGKSTL
31. INGFGRIGR
32. IREGGRTVG
33. IVGESGSGKS
34. KFSTYATWWI
35. KMSKSKGN
36. KMSKSLGN
37. KNMITGAAQMDGAILVV
38. KPNSALRK
39. LFGGAGVGKTV
40. LGPSGCGK
41. LHAGGKFD
42. LIDEARTPLIISG
43. LLNRAPTLH
44. LPDKAIDLIDE
45. LPGKLADC
46. LSGGQQQR
47. MGHVDHGKT
48. NADFDGDQMAVH
49. NGAGKSTL
50. NLLGKRVD
51. NTDAEGRL
52. PSAVGYQPTLA
53. QRVAIARA
54. QRYKGLGEM
55. RDGLKPVHRR
56. SALDVSIQA
57. SGGLHGVG
58. SGSGKSSL
59. SGSGKSTL
60. SVFAGVGERTREGND
61. TGRTHQIRVH
62. TGVSGSGKS
63. TLSGGEAQRI
64. TNKYAEGYP
65. TPRSNPATY
66. VEGDSAGG
67. VRKRPGMYIG

7. A method of identifying genes having functional signatures in the SARS virus, said method comprising steps of:
   a. generating heptapeptide libraries of non-SARS virus genomes with peptide of length 'N' computationally arranged in an alphabetical order,
   b. artificially translating the SARS virus genome to obtain peptide,
   c. identifying the six reading frames in the peptide on the basis of overlappings with the heptapeptide libraries,
   d. converting each peptide sequence into an alphanumeric sequence with one corresponding to each reading frame,
   e. training Artificial Neural Network (ANN) with sigmoidal learning function to the alphanumeric sequence,
   f. deciphering the protein coding regions in the SARS virus genome, and
   g. identifying invariant peptides of SARS virus serving as functional signatures.
8. A method as claimed in claim 7, wherein the method discloses 15 protein-coding regions.
9. A method as claimed in claim 7, wherein the method identifies four novel genes SARS174, SARS68, SARS61, and SARS90.
10. A method as claimed in claim 7, wherein the ANN has one or more input layer, one or more hidden layer with varying number of neurons, and one or more output layer.
11. A method as claimed in claim 7, wherein the number of neurons is preferably 30.
12. A method as claimed in claim 7, wherein the length of the 'N' is 4 or more.
13. A method as claimed in claim 7, wherein the sigmoidal learning function has five parameters comprising total score, mean, fraction of zeroes, maximum continuous non-zero stretch, and variance.
14. A method as claimed in claim 7, wherein the method is better than the conventional methods.
15. A Sars174 gene of SARS virus of SEQ ID No. 1.
16. A Sars gene as claimed in claim 15, wherein the length of the gene is 525 bp.

17. A Sars174 protein of SARS virus of SEQ ID No. 2.
18. A Sars174 protein as claimed in claim 17, wherein the length of the protein is 174 aa.
19. A Sars68 gene of SARS virus of SEQ ID No. 3.
20. A Sars gene as claimed in claim 19, wherein the length of the gene is 207 bp.
21. A Sars68 protein of SARS virus of SEQ ID No. 4.
22. A Sars68 protein as claimed in claim 21, wherein the length of the protein is 68 aa.
23. A Sars61 gene of SARS virus of SEQ ID No. 5.
24. A Sars gene as claimed in claim 23, wherein the length of the gene is 186 bp.
25. A Sars61 protein of SARS virus of SEQ ID No. 6.
26. A Sars61 protein as claimed in claim 25, wherein the length of the protein is 61 aa.
27. A method of drug development in the management in a disease condition, said method comprising step of using a proposed drug for blocking the functioning of one or more invariant peptides as functional signatures identified by the method of claim 1.
28. A method of drug development in the management of SARS virus, said method comprising step of using a proposed drug for blocking the functioning of one or more invariant peptides as functional signatures selected from a group comprising Sars174, Sars68, Sars61, and Sars90.
29. A method as claimed in claim 28, wherein the Sars174 is involved in ABC transporter ATP binding protein.
30. A method as claimed in claim 28, wherein the Sars68 is a major facilitator superfamily protein.
31. A method as claimed in claim 28, wherein the Sars90 is involved in NADH Dehydrogenase I chain.
32. A microprocessor based system for performing the methods of the invention which comprises:
    - determining the amino acid sequence window for creation of peptide library and subsequent origin tagging,
    - comparing the peptide library,

- locating computationally these common peptides in the original proteins and subsequently labeling them with their origin and location, and
- joining computationally the overlapping common peptides to obtain a long chain of invariant peptide sequences,

33. A computer based system for performing the methods of the invention further comprising a central processing unit, executing peptide library creating program (PEPLIB), peptide library matching program (PEPLIMP), peptide stitching program (PEPSTITCH), peptide extraction program (PEPXTRACT) wherein the said programs are all stored in a memory device accessed by the central processing unit connected to a display on which the central processing unit displays the creens of the above mentioned programs in response to user inputs with a user interface device.